Microbial Source Tracking Data

Michael Powell¹, Martin Chandler², Charles Hagedorn³ 16 November 2015

¹EA Engineering, Science, and Technology, Inc., PBC ²Washington Suburban Sanitary Commission ³Virginia Tech



Washington Suburban Sanitary Commission





Background

- Sanitary Sewer Overflow Consent Decree
- Negotiated over several years, entered in Court December 2005
- Water Quality Monitoring Plan
 - Total bacteria
 - Bacterial source tracking : an emerging technology
- WSSC commissioned "White Paper" to identify state-of-the-art BST technologies

Consent Decree

• No guidance or rationale for:

- Selection of sampling points
- Stream flow conditions
- Analytical methods
- Criterion for expected reduction in human source bacteria following collection system repair, rehabilitation, or replacement

WQM Plan

• Monitoring scope:

- 26 sewer basins (annual sampling)
- Semi-annual sampling (20 sewer basins)
- Prepared by EA Engineering:
 - Selected BOX-PCR for MST analyses
 - Identified sampling stations, stream flow criterion
- Quarterly reporting format:
 - Alphabetical by sewer basin name
 - Data in columns for BST and total bacteria values

WQM Implementation

• Underway since March 2007

- Voluntary quarterly sampling in selected Anacostia River sewer basins 2007–2011 (→ not statistically different)
- Added MST "toolbox" tests: fluorescence, human bacteroides HF183
- Nine years of data (thru March 2015):
 - No mandate to evaluate findings or trends
 - EA Engineering prepared two data reports
 - Sewer system rehab. completed in 2 basins, still underway in others

Strong Seasonality



Average Percent Source Contributions of Fecal Bacteria in Surface Waters of Prince George's County and Montgomery County



Human Detections – Montgomery County



Human Detections – Prince George's County





Average Seasonal Source Allocations



MDE's BST Study in Anacostia River, Watershed

- MDE conducted surface water sampling at 6 stations in 2002/2003
 - WSSC collects data at same locations
- Samples collected monthly for period of 1 year
 - Mix of low flow and high flow conditions
- BST conducted using Antibiotic Resistance Analysis (ARA) by Salisbury University
- BST results used for TMDL Allocations

MDE's BST in Anacostia River Watershed

Source Categories:

- Human
- Domestic Animal = dog
- Livestock = horse, pig, goat, sheep, chicken, cow
- Wildlife = goose, deer, rabbit, fox
- Unknown







MDE's BST in Anacostia River Watershed

Average Percent Allocations in MDE's Study

Station ID	Human	Domestic	Livestock	Wildlife	Unknown
BED0001	9.1	27.7	5.6	19.7	38
INC0030	17.3	22.5	9.9	24.4	25.9
NEB0002	6.6	17.3	20.1	26.7	29.3
NWA0002	10.4	19.4	4.8	27.3	38.1
NWA0135	36.4	18.8	3.7	7.7	33.3
PNT0001	16.3	20.4	5.3	29	29

Comparison to MDE's BST in Anacostia₁₄ River Watershed: Beaverdam Creek

WSSC Station UBD001

MDE Station BED0001



Comparison to MDE's BST in Anacostia River Watershed: Indian Creek



MDE Station INC0030



Comparison to MDE's BST in Anacostia River Watershed: Paint Branch



Comparison to MDE's BST in Anacostia River Watershed: Northeast Branch

WSSC Station NEB002

MDE Station NEB0002



Comparison to MDE's BST in Anacostia River Watershed: Northwest Branch Upstream



Comparison to MDE's BST in Anacostia River Watershed: Northwest Branch Downstream



Source Contributions used for TMDL₂₀ Allocations

Allocation Category	Human	Domestic Animals	Livestock	Wildlife
WWTP	Х		X^1	
MS-4		Х		Х
LA	Х		Х	Х

1. Special condition for USDA treatment plant

TMDL Reduction Targets

Maximum Practicable Reduction Targets

Human	Domestic	Livestock	Wildlife
95%	75%	75%	0%

TMDL Reduction Targets

Station	% Domestic Animals	% Human	% Livestock	% Wildlife	% Target Reduction
BED0001	98%	98%	98%	81%	91%
INC0030	98%	98%	98%	<mark>66%</mark>	88%
PNT0001	98%	98%	98%	72%	87%
NEB0002sub	98%	95%	98%	49%	79%
NWA0135	98%	98%	98%	14%	88%
NWA0002sub	98%	98%	98%	53%	78%

Conclusions

- Often unreasonable to reduce non-human microbial loads by 90% as required in some MS4 permits
 - Stormwater BMPs have limited/contradictory data on bacterial reduction
- The ARA Method used by MDE to develop load allocations likely underestimates wildlife contributions
- Genetic-based MST methods have replaced ARA, and have become reasonably inexpensive
- Counties with fecal bacteria TMDLs could benefit from MST by better characterizing human versus non-human sources

Questions?

.3.2: DC Final Average Bacteria Source Distribution for Anacostia Wat am of the NWB and NEB Confluence and Upstream of the Maryland/D

Source ategory	Domestic Animals	Human	Livestock	Wildlife	Total
%	21.1%	22.2%	0.3%	56.5%	100.0

